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OM protein - protein search, using sw model

Run on: August 28, 2002, 17:40:41 ; Search time 20.26 Seconds

(without alignments)  
403.249 Million cell updates/sec

Title: US-09-502-984B-6

Perfect score: 1098

Sequence: 1 KFESKALLAARCPEDLCF.....AEPSFGFWMSMSEPVSLLT 211

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1060	96.5	508	1	EPOR_HUMAN
2	877.5	79.9	507	1	EPOR_RAT
3	869.5	79.2	507	1	EPOR_MOUSE
4	171	15.6	625	1	TPOR_MOUSE
5	146	13.3	635	1	TPOR_HUMAN
6	118	10.7	581	1	PRLR_BOVIN
7	112.5	10.2	634	1	PRLR_BOVIN
8	111	10.1	522	1	IL9R_HUMAN
9	110.5	10.1	634	1	GHR_SHEEP
10	108	9.8	581	1	PRLR_CEREL
11	107	9.7	608	1	GHR_CHICK
12	104.5	9.5	611	1	GHR_COLLI
13	104	9.5	616	1	PRLR_RABIT
14	103.5	9.4	650	1	GHR_MOUSE
15	103.5	9.4	631	1	PRLR_CHICK
16	103	9.4	638	1	GHR_PIG
17	99.5	9.0	638	1	GHR_RABIT
18	99	9.0	831	1	PRLR_MEIGA
19	98.5	9.0	830	1	PRLR_COLLI
20	98	8.9	897	1	CYRB_HUMAN
21	96.5	8.8	378	1	IL3R_HUMAN
22	96	8.7	1165	1	LEPR_HUMAN
23	94	8.6	468	1	IL9R_MOUSE
24	92.5	8.4	638	1	GHR_RAT
25	92	8.4	2594	1	7LBS_DROVI
26	91	8.3	608	1	PRLR_MOUSE
27	89	8.1	638	1	GHR_MACMU
28	88	8.0	622	1	PRLR_HUMAN
29	87	7.9	610	1	PRLR_RAT
30	85.5	7.8	863	1	AMPN_CAUCR
31	85	7.7	184	1	MPL_MPLV
32	84	7.7	336	1	CD11_MOUSE
33	84	7.7	485	1	HXKB_YEAST

34	83.5	7.6	1097	1	LIFR_HUMAN
35	83	7.6	710	1	IRAL_MOUSE
36	83	7.6	805	1	SUSY_SOYBN
37	83	7.6	976	1	EP2A_HUMAN
38	82	7.5	805	1	SUSY_PHAU
39	81	7.4	896	1	CYRB_MOUSE
40	80.5	7.3	459	1	IL7R_MOUSE
41	79.5	7.2	323	1	DIM1_CAEL
42	79.5	7.2	467	1	IL6A_PIG
43	79	7.2	372	1	CNTR_HUMAN
44	79	7.2	485	1	HXKA_YEAST
45	79	7.2	630	1	PRLR_ORENI

## ALIGNMENTS

RESULT ID	1	EPOR_HUMAN	STANDARD:	PRT:	508 AA.
AC	P19235;				
DT	01-NOV-1990 (Rel. 16, Created)				
DT	01-NOV-1990 (Rel. 16, Last sequence update)				
DT	01-MAR-2002 (Rel. 41, Last annotation update)				
DE	Erythropoietin receptor precursor (EPO-R).				
GN	EPOR.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_Taxid=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE-91372359; PubMed-1654273;				
RA	Ehrenman K., St John T.;				
RT	"The erythropoietin receptor gene: cloning and identification of				
RT	multiple transcripts in an erythroid cell line OCIM1.";				
RL	Exp. Hematol. 19:973-977(1991).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE-90304340; PubMed-2163696;				
RA	Jones S.S., D'Andrea A., Haines L.L., Wong G.G.;				
RT	"Human erythropoietin receptor: cloning, expression, and biologic				
RT	characterization.";				
RL	Blood 76:31-35(1990).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Placenta;				
RX	MEDLINE-92399733; PubMed-1668606;				
RA	Noguchi C.T., Bae K.S., Chin K., Wada Y., Schechter A.N.,				
RT	Hankins W.D.;				
RT	"Cloning of the human erythropoietin receptor gene.";				
RL	Blood 78:2548-2556(1991).				
RN	[4]				
RP	SEQUENCE OF 1-96 FROM N.A.				
RC	TISSUE=Placenta;				
RX	MEDLINE-92399734; PubMed-1668607;				
RA	Maouche L., Tournamille C., Hattab C., Boffa G., Carton J.P.,				
RT	Chretien S.;				
RT	"Cloning of the gene encoding the human erythropoietin receptor.";				
RL	Blood 78:2557-2563(1991).				
RN	[5]				
RP	SEQUENCE OF 1-17 FROM N.A.				
RX	MEDLINE-92147143; PubMed-1664413;				
RA	Penny L.A., Forget B.G.;				
RT	"Genomic organization of the human erythropoietin receptor gene.";				
RN	Genomics 11:974-980(1991).				
RP	X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 34-244.				
RX	MEDLINE-96291992; PubMed-8662530;				
RA	Livnah O., Stura E.A., Johnson D.L., Middleton S.A., Mulcahy L.S.,				
RT	Wrighton N.C., Dower W.J., Jolliffe L.K., Wilson I.A.;				
RT	"Functional mimicry of a protein hormone by a peptide agonist: the				
RT	EPO receptor complex at 2.8 A.";				

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RL Science 273:464-471(1996).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 34-244.
RX MEDLINE=99023198; PubMed=9808045;
RA Livneh O., Johnson D.L., Stura E.A., Farrell F.X., Barbone F.P.,
RA Jolliffe L.K., Wilson I.A.;
RA You Y., Liu K.D., Goldsmith M.A., He W., Krause C.D., Festha S.,
RA Jolliffe L.K., Wilson I.A.;
RT "An antagonist peptide-EPO receptor complex suggests that receptor
RT dimerization is not sufficient for activation.";
RL Nat. Struct. Biol. 5:993-1004(1998).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 32-244 IN COMPLEX WITH EPO.
RX MEDLINE=98445092; PubMed=9774108;
RA Syed R.S., Reid S.W., Li C., Cheetham J.C., Aoki K.H., Liu B.,
RA Zhan H., Osslund T.D., Chirino A.J., Zhang J., Finer-Moore J.,
RA Elliott S., Stoney K., Katz B.A., Matthews D.J., Wendoloski J.J.,
RA Egrie J., Stroud R.M.;
RT "Efficiency of signalling through cytokine receptors depends
RT critically on receptor orientation.";
RL Nature 395:511-516(1998).
CC -1- FUNCTION: RECEPTOR FOR ERYTHROPOIETIN. MAY PLAY A ROLE IN THE
CC MECHANISM OF ERYTHROPOIETIN-INDUCED ERYTHROBLAST PROLIFERATION
CC AND DIFFERENTIATION.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -----
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CC -----
DR EMBL: M34986; AA52401.1; -
DR EMBL: M60459; AA52403.1; -
DR EMBL: S45332; AA823271.1; -
DR EMBL: M76595; AA52393.1; -
DR EMBL: M77244; AA52392.1; -
DR PIR: A43799; A43799.
DR PIR: A49824; A49824.
DR PIR: A53958; A53958.
DR PDB: 1EBP; 29-JUL-97.
DR PDB: 1EBA; 18-NOV-98.
DR PDB: 1EER; 01-OCT-99.
DR PDB: 1CN4; 11-AUG-99.
DR MIM: 133171; -
DR InterPro: IPR002996; CRI1.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003528; Hematopo_receptor_L_F1.
DR Pfam: PF00041; fn3; 1.
DR SMART: SM00060; FN3; 1.
DR PROSITE: PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; 3D-structure.
FT SIGNAL 1 24
FT CHAIN 25 508 ERYTHROPOIETIN RECEPTOR.
FT DOMAIN 25 250 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 273 273 POTENTIAL.
FT DOMAIN 274 508 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 148 213 FIBRONECTIN TYPE-III.
FT DISULFID 52 62
FT DISULFID 91 107
FT CARBOHYD 76 76 N-LINKED (GLCNAC....) (POTENTIAL).
SQ SEQUENCE 508 AA; 55065 MW; F9F326E162E9512A CRC64;

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Query Match 96.5%; Score 1060; DB 1; Length 508;
Best Local Similarity 93.8%; Pred. No. 5.7e-96;
Matches 198; Conservative 11; Mismatches 2; Indels 0; Gaps 0;

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1 KFSKKAALLAARGPEELCTERIEDLVCFEEAASAGVGNGNSFSQLEDEPWKLCRL 60
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DB 34 KFSKKAALLAARGPEELCTERIEDLVCFEEAASAGVGNGNSFSQLEDEPWKLCRL 93
QY 61 HQAPTANGAIRFWCSLPTADTSSFVPLERLTAAGAPRRHVRHINEVLLDAPVGLVA 120
DB 94 HQAPTANGAIRFWCSLPTADTSSFVPLERLTAAGAPRRHVRHINEVLLDAPVGLVA 153
QY 121 RLADDSGHVIVRWLPPEPTMTSHIRFELDISAGNGAGSVQVRELLGRTCEVLSNIGR 180
DB 154 RLADDSGHVIVRWLPPEPTMTSHIRFELDISAGNGAGSVQVRELLGRTCEVLSNIGR 213
QY 181 TRITIAVRARMAEPSPFGFWSAMSEPSVLLT 211
DB 214 TRYFAVRARMAEPSPFGFWSAMSEPSVLLT 244

RESULT 2
EPOR_RAT STANDARD; PRT; 507 AA.
AC 007303;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Erythropoietin receptor precursor (EPO-R).
GN EPOR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9326574; PubMed=7684373;
RA Masuda S., Nagao M., Takahata K., Konishi Y., Gallys F.,
RA Tabita T., Sasaki R.;
RT "Functional erythropoietin receptor of the cells with neural
RT characteristics. Comparison with receptor properties of erythroid
RT cells.";
RL J. Biol. Chem. 268:11208-11216(1993).
CC -1- FUNCTION: RECEPTOR FOR ERYTHROPOIETIN. MAY PLAY A ROLE IN THE
CC MECHANISM OF ERYTHROPOIETIN-INDUCED ERYTHROBLAST PROLIFERATION
CC AND DIFFERENTIATION.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -----
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CC -----
DR EMBL: D13566; BAA02761.1; -
DR PIR: A46713; A46713.
DR HSP: P19235; 1EBA.
DR InterPro: IPR002996; CRI1.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003528; Hematopo_receptor_L_F1.
DR Pfam: PF00041; fn3; 1.
DR SMART: SM00060; FN3; 1.
DR PROSITE: PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 507 ERYTHROPOIETIN RECEPTOR.
FT DOMAIN 25 249 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 250 272 POTENTIAL.
FT DOMAIN 273 507 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 147 212 FIBRONECTIN TYPE-III.
FT DISULFID 52 62 BY SIMILARITY.
FT DISULFID 90 106 BY SIMILARITY.
FT CARBOHYD 75 75 N-LINKED (GLCNAC....) (POTENTIAL).
SQ SEQUENCE 507 AA; 55499 MW; AC79AF22D06A7312 CRC64;

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	Query Match	79.9%.	Score 877.5;	DB 1.5;	Length 507;	
	Best Local Similarity	78.2%.	Pred. NO. 3.8e-78;			
	Matches 165; Conservative	23;	Mismatches 22;	IndeIs	1;	Gaps 1.
QY	1 KFEESKAALLIARGPELLCFTERLEDIVCFEEBAASAGVGPENFSFQLEDEPMKICRL	60				
Db	34 KFESKAALLIARGSEELLCFTORLEDIVCFEWEANSGMG-FNYSFYQLGEBSRKSCL	92				
QY	61 HOAPPARCAITFPWCSLPADTSSFPPLDELRLTAAGCAPRFHHVITHINEVLLDAPGLVA	120				
Db	93 HQAPPRKSMRWCSLPPADRSSFPPLDLQVYEAGSGSPRYKHITHINEVLLDAPGLLA	152				
QY	121 RLADESGHVIRIMLPPEPMTSHIRFELDISAGNCAGSVQRVELLEGTECVLSNLRR	180				
Db	153 RRAEGSHVLRMLPDPGAPMTHIRIEVDVASGRAGGTQREVEVLGETECVLSNLRG	212				
QY	181 TRITIAVARARAAEPSEFGFSMSMEPSVSLTT	211				
Db	213 TRYTFVARARAAEPSEFGFSMSMEPSASTLT	243				

RESULT	3
EPOR_MOUSE	STANDARD; PRT; 507 AA.
ID	EPOR_MOUSE
AC	P14753; Q63852;
DT	01-APR-1990 (Rel. 14, Created)
DT	01-APR-1990 (Rel. 14, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last annotation update)
DE	Erythropoietin receptor precursor (EPO-R).
GN	EPO-R.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	MEDLINE=89195238; PubMed=2539263;
RT	D'Andrea A.D., Lodish H.F., Wong G.G.;
RL	"Expression cloning of the murine erythropoietin receptor.";
RL	Cell 57:277-285(1989).
RN	[2]
RP	SEQUENCE FROM N.A.
RA	STRAIN=BALE/C; TISSUE=Liver;
RC	Kuramochi S., Ikawa Y., Todokoro K.;
RX	MEDLINE=91080149; PubMed=2175560;
RT	"Characterization of murine erythropoietin receptor genes.";
RL	J. Mol. Biol. 216:567-575(1990).
RN	[3]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=92017832; PubMed=1656233;
RA	Hino M., Tojo A., Misawa Y., Morii H., Takaku F., Shibuya M.;
RT	"Unregulated expression of the erythropoietin receptor gene caused by
RT	insertion of spleen focus-forming virus long terminal repeat in a
RL	murine erythroleukemia cell line.";
RL	Mol. Cell. Biol. 11:5527-5533(1991).
RN	[4]
RP	SEQUENCE OF 1-27 FROM N.A.
RX	MEDLINE=90287158; PubMed=2162479;
RA	Yousoufian H., Zon L.I., Orkin S.H., D'Andrea A.D., Lodish H.F.;
RT	"Structure and transcription of the mouse erythropoietin receptor
RT	gene.";
RL	Mol. Cell. Biol. 10:3675-3682(1990).
RN	[5]
RP	SEQUENCE OF 1-24 FROM N.A.
RX	MEDLINE=91201346; PubMed=1849897;
RA	Lacombe C., Christien S., Lemarchandel V., Mayeux P., Romeo P.H.,
RA	Gisselbrecht S., Carton J.P.;
RT	"Spleen focus-forming virus long terminal repeat insertional
RT	activation of the murine erythropoietin receptor gene in the T3C1-2
RL	friend leukemia cell line.";
RL	J. Biol. Chem. 266:6952-6956(1991).
RN	[6]

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RX MUTAGENESIS.
RA MEDLINE-93180826; PubMed-8382775;
RA Milra O., Cleveland J.L., Ihle J.N.;
RT "Inactivation of erythropoietin receptor function by point mutations
RT in a region having homology with other cytokine receptors.";
RL Mol. Cell. Biol. 13:11788-1795(1993).
CC -1- FUNCTION: RECEPTOR FOR ERYTHROPOIETIN. MAY PLAY A ROLE IN THE
CC MECHANISM OF ERYTHROPOIETIN-INDUCED ERYTHROBLAST PROLIFERATION
CC AND DIFFERENTIATION.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC
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DR EMBL; J04843; AAA37571.1; -
DR EMBL; X53081; AAA37248.1; -
DR EMBL; M38133; AAA37572.1; -
DR EMBL; M62360; AAA37582.1; -
DR EMBL; S59388; AAB20029.2; -
DR PIR; A32385; A32385.
DR PIR; A41685; A41686.
DR PIR; S13249; S13249.
DR PIR; S14081; S14081.
DR HSSP; P19235; 1EBA.
DR MGD; MGI:95408; Epor.
DR InterPro: IPR002966; CRA.
DR InterPro: IPR003561; FN.III.
DR InterPro: IPR003528; Hematopo_receptor_L.F1.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01352; HEMATOPO_REC_L.F1; 1.
DR Receptor; Transmembrane; Glycoprotein; Signal.
KW SIGNAL
FT CHAIN 1 24
FT DOMAIN 25 507 ERYTHROPOIETIN RECEPTOR.
FT TRANSMEM 250 249 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 273 507 POTENTIAL.
FT DOMAIN 147 212 CYTOPLASMIC (POTENTIAL).
FT DISULFD 52 62 FIBRONECTIN TYPE-III.
FT DISULFD 90 106 BY SIMILARITY.
FT CARBOHD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLCT 291 291 E -> D (IN REF. 3; AAB20029).
SQ SEQUENCE 507 AA; 55194 MW; 067657A2E26451CA CRC64;

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[illegible]

ID	TPOR_MOUSE	STANDARD:	PRT:	625 AA.
4	TPOR_MOUSE			
DT	008351.			
DT	01-FEB-1995 (Rel. 31, Created)			
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Thrombopoietin receptor precursor (TPOR-R) (Myeloproliferative leukemia protein) (C-mpl).			
GN	MPL OR TPOR.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10990;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93327753; PubMed=8334987;			
RA	Skoda R.C., Seldin D.C., Chiang M.K., Peichel C.L., Vogt T.F.,			
RA	Leder P.;			
RT	"Murine c-mpl: a member of the hematopoietic growth factor receptor			
RT	superfamily that transduces a proliferative signal.";			
RL	EMBO J. 12:2645-2653(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=ICF; Tissue=Fetal liver;			
RX	MEDLINE=93390934; PubMed=8397366;			
RA	Vignon I., Florindo C., Fichelson S., Guenet J.-L., Mattel M.-G.,			
RA	Souyri M., Cosman D., Gisselbrecht S.;			
RT	"Characterization of the murine Mpl proto-oncogene, a member of the			
RT	hematopoietic cytokine receptor family: molecular cloning,			
RT	chromosomal location and evidence for a function in cell growth.";			
RL	Oncogene 8:2607-2615(1993).			
CC	-1- FUNCTION: RECEPTOR FOR THROMBOPOIETIN. MAY REPRESENT A REGULATORY			
CC	MOLECULE SPECIFIC FOR TPO-R-DEPENDENT IMMUNE RESPONSES.			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.			
CC	-1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.			
CC	-----			
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CC	-----			
DR	EMBL; 222649; CA80365.1; -;			
DR	EMBL; 222657; CA80372.1; -;			
DR	EMBL; X73677; CA852031.1; -;			
DR	PIR; S35317; S35317.			
DR	HSSP; P19235; IEBA.			
DR	MCD; MGI:97076; Mpl.			
DR	InterPro: IPR002996; CRIA.			
DR	InterPro: IPR003961; FN.III.			
DR	InterPro: IPR003528; Hematopo_receptor_L.F1.			
DR	Plan; PF00041; In3; 1.			
DR	SMART; SMO0060; FN3; 1.			
DR	PROSITE; PS01352; HEMATOPO_REC_L.F1; 1.			
KW	Receptor; Transmembrane; Glycoprotein; Signal; Repeat.			
FT	CHAIN	1	25	POTENTIAL.
FT	CHAIN	26	625	THROMBOPOIETIN RECEPTOR.
FT	DOMAIN	26	482	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	483	504	POTENTIAL.
FT	DOMAIN	505	625	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	117	117	N-LINKED (GLCNAc. . .) (POTENTIAL).
FT	CONFLICT	2	8	MISSING (IN REF. 2).
FT	CONFLICT	99	99	D -> V (IN REF. 2).
FT	CONFLICT	222	222	P -> P (IN REF. 2).
SO	SEQUENCE	625 AA;	69817 MW;	309CFEAA3724549 CRC64;

Matches 62; Conservative 33; Mismatches 105; Indels 52; Gaps 8

OY 4 STRALLANGPELLCTFRLIEDLYCFEEEASAGCPNFSFQLEDEPMKLCRLHA 63  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db 25 SDVFLAIGTPEPLNCFSQTFEDLFCFMWEEBAA--PSGTOLLYAVRGEKPACPLYSO 82  
OY 64 PARGAIRFWCSLPPAD--TSFVPLELRITLAS-GAPRRRIHINEVYLDPAGVLAR 121  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db 83 SVPTGTRIVCCFPADDEVRLFELFLHWKNVNSLNQTLQRVLFDVSGLPAPRVIKAR 142  
OY 122 IADESHVVIRN-LPPETPMTSHIRFELDI---SAGNGAGSVORVELLEGRT----- 170  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db 143 GGSQGGELQIHMEADAPE--ISDFLRHELRYGPPTSNNATFSV--IQLSTETCCPLM 198  
OY 171 -----ECVLSNRGRTRTTIAVRARMAPSIC 197  
Db 199 MENPVYLDOPPCVHTPASQPHGPAPEFLTVKGSGCLVSLGASKSXYMLQRSQPGVSLR 258  
OY 198 GFWSAMSEPVSL 209  
| | | | : : : :  
Db 259 GSMGSPSPVTY 270

RESULT 5  
TPOR\_HUMAN  
ID TPOR\_HUMAN STANDARD: PRT: 635 AA.  
AC P40238;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DE 16-OCT-2001 (Rel. 40, Last annotation update)  
PR Thrombopoietin receptor precursor (PRO-R) (Myeloproliferative leukemia protein) (C-MPL) (CD110 antigen).  
GN MPL OR TPOR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92302297; PubMed=1608974;  
RA Vigon I., Morron J.-P., Coccault L., Mitjavila M.-T., Tamboulin P., Giselsbrecht S., Souyri M.;  
RT "Molecular cloning and characterization of MPL, the human homolog of the v-mpl oncogene: Identification of a member of the hematopoietic growth factor receptor superfamily.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:5640-5644(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94292186; PubMed=8020956;  
RA Migotte V., Vigon I., de Crevecoeur E., Romeo P.H., Lemarchandel V., Christien S.;  
RT "Structure and transcription of the human c-mpl gene (MPL)." ;  
RL Genomics 20:5-12(1994).  
CC -I- FUNCTION: RECEPTOR FOR THROMBOPOIETIN. MAY REPRESENT A REGULATORY MOLECULE SPECIFIC FOR TPO-R-DEPENDENT IMMUNE RESPONSES.  
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -I- ALTERNATIVE PRODUCTS: 2 ISOFORMS: C-MPL-K (SHOWN HERE) AND C-MPL-P; ARE PRODUCED BY ALTERNATIVE SPLICING.  
CC -I- TISSUE SPECIFICITY: EXPRESSED AT A LOW LEVEL IN A LARGE NUMBER OF CELLS OF HEMATOPOIETIC ORIGIN. THE TWO FORMS (C-MPL-K AND C-MPL-P) ARE ALWAYS FOUND TO BE COEXPRESSED.  
CC -I- DISEASE: DEFECTS IN MPL ARE A CAUSE OF CONGENITAL AMEGAKARYOCYTIC THROMBOCYTOPENIA (CAMT); A DISEASE CHARACTERIZED BY ISOLATED THROMBOCYTOPENIA AND MEGAKARYOCYTOPENIA WITH NO PHYSICAL ANOMALIES.  
CC -I- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
CC -I- SIMILARITY: CONTAINS 2 FIBROBLAST TYPE III-TYPE DOMAINS.  
CC -I- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-8 IS THE INITIATOR.  
CC -I- DATABASE: NAME=PROW; NOTE=Cd guide CD110 entry;  
CC WWW:"http://www.ncbi.nlm.nih.gov/prov/guide/11586825.g.htm".  
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Qy	117	GVALL---	ADSSGVVYRWLPPEPTPMTSH---	TFREFLDISAGNGASGVQVCELEERT	170
Db	132	NITLELKHPEDRKPLINKSPPTMDVKS	SGCFITLQYELRLKPEKATMETHFTLKQ--T	189	
Qy	171	ECVLSNLGRFRTITIAVARARMAE	SPSGFGFWASAMSEPVSL	209	
Db	190	OLKIFNLVPGKLYVOIRCK---	PDH-GYWSFWSPESSI	224	
RESULT	7				
ID	GHR_BOVIN	STANDARD;	PRT;	634 AA.	
AC	P79108;				
DT	01-NOV-1997 (Rel. 35, Created)				
DT	01-NOV-1997 (Rel. 35, Last sequence update)				
DT	01-NOV-1997 (Rel. 35, Last annotation update)				
DE	Growth hormone receptor precursor (GH receptor) (Serum binding protein).				
DE	GHR.				
OS	Bos taurus (Bovine).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;				
OC	Bovidae; Bovinae; Bos.				
OX	NCBI_TaxID=9913;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=GI; TISSUE=Liver;				
RA	Souza S.C., Wang X., Lobo R.B., Kopechick J.J.;				
RL	Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.				
CC	- FUNCTION: THIS IS A RECEPTOR FOR PITUITARY GLAND GROWTH HORMONE.				
CC	- SUBUNIT: HOMODIMER (BY SIMILARITY).				
CC	- SUBCELLULAR LOCATION: Type I membrane protein.				
CC	- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.				
CC	- SIMILARITY: CONTAINS 1 FIBROBLAST TYPE III-LIKE DOMAIN.				
CC	-----				
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CC	use by non-profit institutions as long as its content is in no way				
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CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> ).				
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).				
CC	-----				
DR	EMBL; X70041; CAA49635.1; -.				
DR	HSSP; P10912; IHWH.				
DR	InterPro; IPR002896; CRA.				
DR	InterPro; IPR003961; FN_III.				
DR	InterPro; IPR003528; Hematopo_receptor_L_FL.				
DR	Pfam; PF00041; fn3; 1.				
DR	SMART; SMO0060; FN3; 1.				
DR	PROSITE; PS01352; HEMATOPO_REC_L_FL; 1.				
FW	Receptor; Transmembrane; Glycoprotein; Signal.				
FT	SIGNAL	1	18	POTENTIAL.	
FT	CHAIN	19	634	GROWTH HORMONE RECEPTOR.	
FT	DOMAIN	19	260	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM	261	284	POTENTIAL.	
FT	DOMAIN	285	634	CYTOPLASMIC (POTENTIAL).	
FT	DOMAIN	141	248	FIBROBLAST TYPE-III.	
FT	DISULFID	56	66	BY SIMILARITY.	
FT	DISULFID	97	108	BY SIMILARITY.	
FT	DISULFID	122	136	BY SIMILARITY.	
FT	CARBOHYD	46	46	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	73	73	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	111	111	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	152	152	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	157	157	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	196	196	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FO	SEQUENCE	634 AA;	70979 MW;	91955kDa2896kDa28 CRG64;	

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OY      14 PEELCEFERLEDLVCEFEDEAAAGV--GGNGS--FSFOLDEPCKICLHOQAPTAARGAIR 71
          | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB       51 PEFWCRSPLEETESCHMTDGNHSLQSPGVQMFYIRRDIOEMKEC-----PDIVSAGE 105
          | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY      72 FWCSTPLTADTSFVLELRITLAASGAPPFHRRIHINEVLLDAPYGVARLADES----- 126
          | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB      106 NSCYNNSSTYSWTMPYCRLKITSNGSIYD-HKCFSVEDIVQDDPPRYGLMWILLINSLTEIH 164
          | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY      127 GHVVIRWLPPPERT 139
          .....| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB      165 ADILVKWEPPPT 177

RESULT   8
IL9R_HUMAN
ID        IL9R_HUMAN           STANDARD;             PRT;              522 AA.
AC        Q01113; Q14634;
DT        01-APR-1993 (Rel. 25, Created)
DF        01-APR-1993 (Rel. 25, Last sequence update)
DE        16-OCT-2001 (Rel. 40, Last annotation update)
DN        Interleukin-9 receptor precursor (IL-9R).
GN        (IL9RX OR IL9R) AND (IL9RY OR IL9R).
OS        Homo sapiens (Human).
OC        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CX        Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxId=9606;
[1]
RN        SEQUENCE FROM N.A.
RX        MEDLINE=92302307; PubMed=1376929;
RA        Renaud J.C., Druze C., Kermouni A., Housiau F., Uyttenhove C.,
RT        van Roost E., van Snick J.;
RT        "Expression cloning of the murine and human interleukin 9 receptor
RT        cDNAs.";
RT        Proc. Natl. Acad. Sci. U.S.A. 89:5690-5694(1992).
[2]
RN        SEQUENCE FROM N.A.
RX        MEDLINE=94250901; PubMed=8193355;
RA        Chang M.S., Engel G., Benedict C., Basu R., McIninch J.;
RT        "Isolation and characterization of the human interleukin-9 receptor
RT        gene.";
RT        Blood 83:3199-3205(1994).
[3]
RN        SEQUENCE FROM N.A.
RP        TISSUE=Melanoma;
RX        MEDLINE=96115587; PubMed=8666384;
RA        Kermouni A., van Roost E., Arden K.C., Vermeesch J.R., Weiss S.,
RA        Godelaine D., Flint J., Lurquin C., Szikora J.P., Higgs D.R.,
RA        Marynen P., Renaud J.C.;
RT        "The IL-9 receptor gene (IL9R): genomic structure, chromosomal
RT        localisation in the pseudautosomal region of the long arm of the sex
RT        chromosomes, and identification of IL9R pseudogenes at 9pter, 10pter,
RT        16pter, and 18pter.";
RL        Genomics 29:371-382(1995).
CC        -1- FUNCTION: THIS IS A RECEPTOR FOR INTERLEUKIN-9.
CC        -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN AND SECRETED.
CC        -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC        -1- SIMILARITY: CONTAINS 1 FIROREECTIN TYPE III-LIKE DOMAIN.
CC        CC
CC        This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC        entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC        or send an email to licens@isb-sib.ch).
DR        EMBL; M84747; AAA58679.1; .
DR        EMBL; S71404; AAB30844.2; ALT_SEQ.
DR        EMBL; S71420; AAD14081.1; .
DR        EMBL; L39064; AAC29513.1; .
DR        PIR; B45268; B45268.
DR        MIM; 300007; .

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DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003531; Hematopo_receptor_S_F1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 40
FT CHAIN 1 522
FT DOMAIN 41 522 INTERLEUKIN-9 RECEPTOR.
FT TRANSMEM 271 291 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 292 522 POTENTIAL.
FT DOMAIN 150 244 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 429 439 FIBRONECTIN TYPE-III.
FT DOMAIN 440 443 POLY-SER.
FT CARBOHYD 117 117 POLY-ASN.
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 331 331 R -> G (IN REF. 3).
FT CONFLICT 439 439 MISSING (IN REF. 3).
SQ SEQUENCE 522 AA; 57333 MW; E6GB5C6342DEB2 CRC64;

Query Match 10.1%; Score 111; DB 1; Length 522;
Best Local Similarity 23.7%; Pred. No. 0.0029;
Matches 53; Conservative 28; Mismatches 97; Indels 46; Gaps 11;

QY 12 KGPPE--LLCTFERLEDVCFEEAASAGVGPNGFSFQLEDEPWKLCRLHQAPTARGA 69
DB 47 QGPRSRFTFLTNMILRIDCHW-SAPELGQ-----SSPWLLFTSNQAPGCTHK 94
QY 70 IRFMCSLPTADSSFPLELRITLTAAG-APRRHYHINEV-----VLLDAP 115
DB 95 ----CILKSGSECTVLPAPAVLVPSPDNTITFHHCMSGREQVSLVDPEYLPRRHVKLDP 150
QY 116 VGLVARLADSEGHVYIRW-LPPETPMTHIRFELDISANGNA-GSVGRVELLEGTECV 173
DB 151 SLOQSNIS--SCHCLTWSISPALERPMTLLSYELAFKQOEAMQAOQRDHIVGTWLI 208
QY 174 LSNL-----RGRRTIAVAR--MAEPSFGGFWASSEPV 207
DB 209 LEAFELDPGFIEARLRYOMATLEDDVEERYTGQWSEMSQPV 252

RESULT 9
GHR_SHEEP STANDARD: PRT; 634 AA.
AC Q28575;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Growth hormone receptor precursor (GH receptor) (Serum binding
DE protein).
DE GHR.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91099608; PubMed=1980117;
RA Adams T.E., Baker L., Fiddes R.J., Brandon M.R.;
RT "The sheep growth hormone receptor: molecular cloning and ontogeny of
RT mRNA expression in the liver."
RL Mol. Cell. Endocrinol. 73:135-145(1990).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR PITUITARY GLAND GROWTH HORMONE.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M82912; AA73171.1; -.
DR HSSP; P10912; IAXI.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003528; Hematopo_receptor_L_F1.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
KW PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 18
FT CHAIN 1 19
FT DOMAIN 19 260 GROWTH HORMONE RECEPTOR.
FT TRANSMEM 261 284 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 285 634 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 141 248 FIBRONECTIN TYPE-III.
FT DISULFID 56 66 BY SIMILARITY.
FT DISULFID 97 108 BY SIMILARITY.
FT DISULFID 122 136 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 634 AA; 70844 MW; FFD2B89C23EC1496 CRC64;

Query Match 10.1%; Score 110.5; DB 1; Length 634;
Best Local Similarity 26.6%; Pred. No. 0.0041;
Matches 34; Conservative 24; Mismatches 57; Indels 13; Gaps 5;

QY 19 CETERLEDVCFEEAASAGV-GPGNFS-FSQLEDEPWKLCRLHQAPTARGAIRFWSL 76
DB 56 CSPELETFSCHWTDGANSLSQSPGSVQMFYIRPDIOEKKC-----PDYVAGENSQYF 110
QY 77 PTADTSSFPLELRITLTAAGAPRRHYHINEVLLDAPVGLVARLADS-----GHVYI 131
DB 111 NSSYSTSWTPYCIKILTSNGIVD-HKCFSEVEDIVQDPDPGLMTWLSTLEIHADILV 169
QY 132 RWLPPPET 139
DB 170 KWPEPPPT 177

RESULT 10
PRLR_CEREL STANDARD: PRT; 581 AA.
AC Q28235;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Prolactin receptor precursor (PRL-R).
DE PRLR.
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96030711; PubMed=7561644;
RA Clarke L.A., Edey M., London A.S., Randall V.A., Postel-Vinay M.C.,
RA Kelly P.A., Jabbour H.N.;
RT "Expression of the prolactin receptor gene during the breeding and
RT non-breeding seasons in red deer (Cervus elaphus): evidence for the
RT expression of two forms in the testis."
RL J. Endocrinol. 146:313-321(1995).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE

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CC PROLACTIN.
CC -1 SUBCELLULAR LOCATION: Type I membrane protein.
CC -1 SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1 SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X94953; CAA64419.1; -.
CC HSSP: P14787; IAN3.
CC InterPro: IPR002996; CRIA.
CC InterPro: IPR003961; FN.III.
CC InterPro: IPR003528; Hematopo_receptor_L_F1.
CC Pfam: PF00041; fn3; 2.
CC SMART: SM00060; fn3; 1.
CC PROSITE: PS01352; HEMATOPO_REC_L_F1; 1.
CC Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
CC FT SIGNAL 1 24
CC FT CHAIN 25 581
CC FT DOMAIN 25 234
CC FT TRANSMEM 235 258
CC FT DOMAIN 259 581
CC FT DOMAIN 25 122
CC FT DOMAIN 123 227
CC FT DISULFID 36 46
CC FT DISULFID 75 86
CC FT CARBOHYD 59 59
CC FT CARBOHYD 132 132
CC FT CARBOHYD 233 233
CC SEQUENCE 581 AA; 65159 MW; 975E47CB63CF28EC CRC64;

Query Match 9.8%; Score 108; DB 1; Length 581;
Best Local Similarity 20.7%; Pred. No. 0.0064;
Matches 43; Conservative 41; Mismatches 98; Indels 26; Gaps 9;

QY 14 PELLCTERLELDVCFEEEAASAGVGPNGFSFOLEDEPWKICRLHOAPFARGAIRFW 73
DB 31 PKIKCRSPKKEFTCTCWMEGSDGL-PTNYTLTYHKEGE-----TLIHEPDKTGKGPNT 85
QY 74 CSLPTADTSSFVLELEFLTA-----ASGAPRFRVTHINEVLLDPAVGLVARL--AD 124
DB 86 CYSKRHTSIWKIYVITVNAINGVSSDPLX---VDVYIYIEPPEPAMLTLELKHPE 142
QY 125 ESGHVIVIRMLPPETPMTS---HIREFLDISAGNGAGSVORVELLEGTCEVLSNLRGT 181
DB 143 RKPYLWKMPPTPLTDVKSQWFMIOYERIKRPTAAD--WEIHFAAKOTLKIIFSLVPG 200
QY 182 RITIAVARARMAEPSPFGFGFMSSEPVS 209
DB 201 KYLVQVACK---PDH-GYNSMSEPESSI 224

RESULT 11
GHR_CHICK ID STANDARD; PRT; 608 AA.
AC 002092;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Growth hormone receptor precursor (GH receptor) (Serum binding
DE protein).
GN GHR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;

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RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91243665; PubMed=2036984;
RA Burnside J, Liou S.S, Copburn L.A.;
RT "Molecular cloning of the chicken growth hormone receptor
RT complementary deoxyribonucleic acid: mutation of the gene in
RT sex-linked dwarf chickens.";
RL Endocrinology 128:3183-3192(1991).
CC -1 FUNCTION: THIS IS A RECEPTOR FOR PITUITARY GLAND GROWTH HORMONE.
CC -1 SUBUNIT: HOMODIMER.
CC -1 SUBCELLULAR LOCATION: Type I membrane protein.
CC -1 TISSUE SPECIFICITY: BROAD SPECIFICITY.
CC -1 SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1 SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M74057; AAA48781.1; -.
CC PIR: S32823; S32823.
CC HSSP: P10912; IHW.
CC InterPro: IPR002996; CRIA.
CC InterPro: IPR003961; FN.III.
CC InterPro: IPR003528; Hematopo_receptor_L_F1.
CC Pfam: PF00041; fn3; 1.
CC SMART: SM00060; fn3; 1.
CC PROSITE: PS01352; HEMATOPO_REC_L_F1; 1.
CC Receptor; Transmembrane; Glycoprotein; Signal.
CC FT SIGNAL 1 16
CC FT CHAIN 17 608
CC FT DOMAIN 17 237
CC FT TRANSMEM 238 261
CC FT DOMAIN 262 608
CC FT DOMAIN 117 223
CC FT DISULFID 34 44
CC FT DISULFID 72 83
CC FT DISULFID 97 111
CC FT CARBOHYD 86 86
CC FT CARBOHYD 127 127
CC FT CARBOHYD 132 132
CC FT CARBOHYD 171 171
CC SEQUENCE 608 AA; 68572 MW; D71AD7B6C62528DC CRC64;

Query Match 9.7%; Score 107; DB 1; Length 608;
Best Local Similarity 26.7%; Pred. No. 0.0085;
Matches 54; Conservative 26; Mismatches 90; Indels 32; Gaps 9;

QY 14 PELLCTERLELDVCFEEEAASAGVGPNGFSFOL-----DDEPWKICRLHOAPFARG 68
DB 29 PQISKCRSPLETFSCWTWD-----GKVTSGTIQLLYKKRSDDEWKEC-----PDYIT 77
QY 69 AIRFWCSLPTADTSSFVLELEFLTAASGAPRFRVTHINEVLLDPAVGLVARLADES-- 126
DB 78 AGNSCYFNSTSYTSIMIPYVKL-ANKDEVFDEKCFSEVDIVLPDPVHLNMTLLNMTNSQT 136
QY 127 ---GHVIVIRMLPPETPMTS---HIREFLDISAGNGAGSVORVELLEGTCEV--LSNR 178
DB 137 GIHQDIDQVMDPPFADVQGWITLLEYELQYKVENET---KKKELEPRISTVVPYLSLK 192
QY 179 GRTIRITAVARARMAEPSPFGGF 199
DB 193 MGRDYELIRVRSRORTSEKGEF 214

RESULT 12
GHR_COLL

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ID  GHR_COLLI          STANDARD;          PRT;          611 AA.
AC  Q90375;
DT  01-NOV-1997 (Rel. 35, Created)
DT  01-NOV-1997 (Rel. 35, Last sequence update)
DT  01-NOV-1997 (Rel. 35, Last annotation update)
DE  Growth hormone receptor precursor (GH receptor) (Serum binding
GN  protein).
OS  Columba livia (Domestic pigeon).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Archosuria; Aves; Neognathae; Columbiformes; Columbidae; Columba.
OX  NCBI_TaxID=8932;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Liver;
RA  Cheng C.H.K., Shaw P.C., Tsim K.W.K., Lau K.F.;
RL  Submitted (JAN-1996) to the EMBL/Genbank/DBJ databases.
CC  -1- FUNCTION: THIS IS A RECEPTOR FOR PITUITARY GLAND GROWTH HORMONE.
CC  -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC  -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC  -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC  -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL: U20353; AAA84745.1; -.
DR  HSSP: P10912; IAXI.
DR  InterPro: IPR002996; CRIA.
DR  InterPro: IPR003961; FN_III.
DR  InterPro: IPR003528; Hematopo_receptor_L_F1.
DR  Pfam: PF00041; fn3; 1.
DR  SMART: SM00060; FN3; 1.
DR  PROSITE: PS01352; HEMATOPO_REC_L_F1; 1.
KW  Receptor; Transmembrane; Glycoprotein; Signal.
FT  SIGNAL 1 20
FT  CHAIN 1 611
FT  DOMAIN 21 240
FT  TRANSMEM 241 264
FT  DOMAIN 265 611
FT  DOMAIN 119 226
FT  DISULFID 34 44
FT  DISULFID 75 86
FT  DISULFID 100 114
FT  CARBOHYD 16 16
FT  CARBOHYD 53 53
FT  CARBOHYD 89 89
FT  CARBOHYD 130 130
FT  CARBOHYD 135 135
FT  CARBOHYD 174 174
SQ  SEQUENCE 611 AA; 68851 MW; C48750BFEE4BDA CRC64;

Query Match 9.5%; Score 104.5; DB 1; Length 611;
Best Local Similarity 26.2%; Pred. No. 0.015;
Matches 53; Conservative 28; Mismatches 96; Indels 25; Gaps 10;

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OY  179 GRTTITAVARAW-AEPSEGEF 199
    | | | | | | |
DB  196 IGDYRIRVRSNORTSEKGEF 217

RESULT 13
PRLR_RABIT
ID  PRLR_RABIT          STANDARD;          PRT;          616 AA.
AC  P14787;
DT  01-APR-1990 (Rel. 14, Created)
DT  01-APR-1990 (Rel. 14, Last sequence update)
DT  15-JUL-1998 (Rel. 36, Last annotation update)
DE  Prolactin receptor precursor (PRL-R).
GN  PRLR.
OS  Oryctolagus cuniculus (Rabbit).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX  NCBI_TaxID=9986;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Mammary gland;
RX  MEDLINE=89184578; PubMed=2928321;
RA  Edey M., Jolicœur C., Levi-Meyrueis C., Dusanter-Fourt I.,
RA  Petridou B., Boutin J.M., Lesueur L., Kelly P.A., Djiane J.;
RT  "Identification and sequence analysis of a second form of prolactin
RT  receptor by molecular cloning of complementary DNA from rabbit
RT  mammary gland.";
RL  Proc. Natl. Acad. Sci. U.S.A. 86:2112-2116(1989).
RN  [2]
RP  3D-STRUCTURE MODELING OF 30-228.
RX  MEDLINE=97248733; PubMed=9094747;
RA  Halaby D., Thoreau E., Djiane J., Morron J.P.;
RT  "Homology modeling of rabbit prolactin hormone complexed with its
RT  receptor.";
RL  Proteins 27:459-468(1997).
CC  -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC  PROLACTIN.
CC  -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC  -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC  -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL: J04510; AAA31457.1; -.
DR  PIR: A30304; A30304.
DR  PDB: 1AN3; 03-DEC-97.
DR  InterPro: IPR002996; CRIA.
DR  InterPro: IPR003961; FN_III.
DR  InterPro: IPR003528; Hematopo_receptor_L_F1.
DR  Pfam: PF00041; fn3; 2.
DR  SMART: SM00060; FN3; 2.
DR  PROSITE: PS01352; HEMATOPO_REC_L_F1; 1.
KW  Receptor; Transmembrane; Glycoprotein; Signal; Repeat; 3D-structure.
FT  SIGNAL 1 24
FT  CHAIN 1 616
FT  DOMAIN 25 616
FT  TRANSMEM 235 258
FT  DOMAIN 259 616
FT  DOMAIN 124 227
FT  DISULFID 36 46
FT  DISULFID 75 86
FT  CARBOHYD 59 59
FT  CARBOHYD 104 104
FT  CARBOHYD 132 132
SQ  SEQUENCE 616 AA; 68840 MW; 800E3166FEF7108C CRC64;

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FT VARSPUBLIC 297 650 MISSING (IN ISOFORM 2).  
 FT CONFLICT 25 25 T -> A (IN REF. 6).  
 FT CONFLICT 162 162 G -> A (IN REF. 3 AND 4).  
 FT CONFLICT 325 325 E -> G (IN REF. 2).  
 FT CONFLICT 423 423 R -> A (IN REF. 2).  
 SQ SEQUENCE 650 AA; 72783 MW; 95653380CAFOB931 CRC64;

Query Match 9.4%; Score 103.5; DB 1; Length 650;  
 Best Local Similarity 22.6%; Pred. No. 0.02; Mismatches 39; Indels 47; Gaps 10;  
 Matches 51; Conservative 39;

QY 14 PERLLCTERLEDLVCFEEAASAGV-GPGNFSFSEFOLED-----EPMKLCR 59  
 DB 51 PRRTKCRSPLELFSCYWMGNDPDKTPGSLDYAKRSGQARIAHEMTQEMKEC- 109  
 QY 60 LHOAPFARGAIRFWCSLPADTSSVPLERLTAASGAPRHHVHINEVLLDAPVGL 119  
 DB 110 ---PQVSAKNSCYENSYSIWIPYCIKLT-TNODLIDQKCFVDEIOPDPPIGLN 164  
 QY 120 ARLADS-----GHVYIRMLPPEPTP-MTSHIRFELDLSAGNGASVQRELLGGR---- 169  
 DB 165 WILNLSLIGIRGDIOVSWOPPNADVLKGMILEYETI-----QYKVENSKWKVM 215  
 QY 170 -----TECVLSNLRGRTITIAVARMAEPSPFGFSWAMSEPVSL 210  
 DB 216 GPWLTYCPYSLRMDKEHEVYRSR--QRSFEKY--SEFEVLRVI 258

RESULT 15  
 PRLR-CHICK STANDARD; PRT; 831 AA.  
 AC 004594;

DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Prolactin receptor precursor (PRL-R) (CPRLP).  
 GN PRLR.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosaurii; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=WHITE LEGHORN; TISSUE=Kidney;  
 RX MEDLINE=93075121; PubMed=1445292;

RA Tanaka M., Maeda K., Okubo T., Nakashima K.;  
 RT "Double antenna structure of chicken prolactin receptor deduced from  
 the cDNA sequence."  
 RL Biochem. Biophys. Res. Commun. 188:490-496(1992).  
 CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE  
 PROLACTIN

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
 CC -!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.

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DR EMBL: D13154; BA002439.1; -  
 DR PIR: J01655; J01655.  
 DR HSSP: P14787; IAN3.  
 DR InterPro: IPR002396; CRIA.  
 DR InterPro: IPR003961; FN\_III.  
 DR InterPro: IPR003528; Hematopo\_receptor\_L\_F1.  
 DR Pfam: PF00041; fn3; 4.  
 DR SMART: SM00060; FN3; 3.

DR PROSITE: PS01352; HEMATOPO\_REC\_L\_F1; 1.  
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.  
 FT SIGNAL 1 23 POTENTIAL.  
 FT CHAIN 24 831 PROLACTIN RECEPTOR.  
 FT DOMAIN 24 438 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 439 459 POTENTIAL.  
 FT DOMAIN 460 831 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 25 122 FIBRONECTIN TYPE-III 1.  
 FT DOMAIN 123 225 FIBRONECTIN TYPE-III 2.  
 FT DOMAIN 228 325 FIBRONECTIN TYPE-III 3.  
 FT DOMAIN 326 428 FIBRONECTIN TYPE-III 4.  
 FT DISULFID 36 46 BY SIMILARITY.  
 FT DISULFID 75 86 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 112 132 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 303 303 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 335 335 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 831 AA; 94102 MW; 1CAE75791DCADBE9 CRC64;

Query Match 9.4%; Score 103.5; DB 1; Length 831;  
 Best Local Similarity 20.0%; Pred. No. 0.027; Mismatches 102; Indels 29; Gaps 8;  
 Matches 42; Conservative 37;

QY 5 KAALLAARGPEELCTERLEDLVCFEEAASAGVPGNFSFSEFOLEDPFKLCRLHOAP 64  
 DB 233 KPTIINCSPK-----EFTCMWKPGDLDG-HPTNTLLYSNGEE--QYEECP 279  
 QY 65 TANGAIRFWCSLPADTSSVPLERLTA-----SGAPRHHVHINEVLLDAPVGL 118  
 DB 280 DVTAGPNSCYFDKKTSTFTIYNITVRATNEMGSNSDPHY--VDVYIYQDPDPVNV 336  
 QY 119 VARL---ADESGHVYIRMLPPEPTPMTS-HIRELDLSAGNGASVQRELLGGRFCV 174  
 DB 337 TLELKPINKKPYLVLWSPPLADYSGWLTLEYELRLKPERGEEMETTFVGQOTQYKK 396  
 QY 175 SNLRGRTITIAVARMAEPSPFGFSWAMS 204  
 DB 397 FSLNPGKKYIIOIHK--PDHGSMSWS 423

Search completed: August 28, 2002, 17:40:42  
 Job time: 533 sec

